

RAW SEQUENCE LISTING

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Application Serial Number: 08/910,449A
Source: IFW/6
Date Processed by STIC: 8/11/06

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 08/11/2006
PATENT APPLICATION: US/08/910,449A **TIME:** 09:40:45

Input Set : A:\2801-C seq listing.txt
Output Set: N:\CRF4\08112006\H910449A.raw

3 <110> APPLICANT: Goodwin, Raymond G.
4 Smith, Craig A.
6 <120> TITLE OF INVENTION: 4-1BB Polypeptides and DNA Encoding 4-1BB Polypeptides
8 <130> FILE REFERENCE: 2801-C
10 <140> CURRENT APPLICATION NUMBER: US 08/910,449A
11 <141> CURRENT FILING DATE: 1997-08-05
13 <150> PRIOR APPLICATION NUMBER: US 08/236,918
14 <151> PRIOR FILING DATE: 1994-05-06
16 <150> PRIOR APPLICATION NUMBER: US 08/060,843
17 <151> PRIOR FILING DATE: 1993-05-07
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1254
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus sp.
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (53)..(979)
32 <223> OTHER INFORMATION: (Clone: murine 4-1BB-L)
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37 1
38 cag cac aca ctt gat gtg gag gat acc gcg gat gcc aga cat cca gca 106
39 Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His Pro Ala
40 5 10 15
41 ggt act tcg tgc ccc tcg gat gcg gcg ctc ctc aga gat acc ggg ctc 154
42 Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr Gly Leu
43 20 25 30
44 ctc gcg gac gct gcg ctc tca gat act gtg cgc ccc aca aat gcc 202
45 Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr Asn Ala
46 35 40 45 50
47 gcg ctc ccc acg gat gct gcc tac cct gcg gtt aat gtt cgg gat cgc 250
48 Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg Asp Arg
49 55 60 65
50 gag gcc gcg tgg ccg cct gca ctg aac ttc tgt tcc cgc cac cca aag 298
51 Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His Pro Lys
52 70 75 80
53 85 90 95
54 ctc tat ggc cta gtc gct ttg gtt ttg ctg ctt ctg atc gcc gcc tgt 346
55 Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Ile Ala Ala Cys
56 85 90 95
57 gtt cct atc ttc acc cgc acc gag cct cgg cca gcg ctc aca atc acc 394

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65 100 105 110		
67 acc tcg ccc aac ctg ggt acc cga gag aat aat gca gac cag gtc acc	442	
68 Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln Val Thr		
69 115 120 125 130		
71 cct gtt tcc cac att ggc tgc ccc aac act aca caa cag ggc tct cct	490	
72 Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly Ser Pro		
73 135 140 145		
75 gtg ttc gcc aag cta ctg gct aaa aac caa gca tcg ttg tgc aat aca	538	
76 Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys Asn Thr		
77 150 155 160		
79 act ctg aac tgg cac agc caa gat gga gct ggg agc tca tac cta tct	586	
80 Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu Ser		
81 165 170 175		
83 caa ggt ctg agg tac gaa gaa gac aaa aag gag ttg gtg gta gac agt	634	
84 Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val Asp Ser		
85 180 185 190		
87 ccc ggg ctc tac tac gta ttt ttg gaa ctg aag ctc agt cca aca ttc	682	
88 Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr Phe		
89 195 200 205 210		
91 aca aac aca ggc cac aag gtg cag ggc tgg gtc tct ctt gtt ttg caa	730	
92 Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu Gln		
93 215 220 225		
95 gca aag cct cag gta gat gac ttt gac aac ttg gcc ctg aca gtg gaa	778	
96 Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val Glu		
97 230 235 240		
99 ctg ttc cct tgc tcc atg gag aac aag tta gtg gac cgt tcc tgg agt	826	
100 Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp Ser		
101 245 250 255		
103 caa ctg ttg ctc ctg aag gct ggc cac cgc ctc agt gtg ggt ctg agg	874	
104 Gln Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu Arg		
105 260 265 270		
107 gct tat ctg cat gga gcc cag gat gca tac aga gac ttg gag ctg tct	922	
108 Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu Ser		
109 275 280 285 290		
111 tat ccc aac acc acc agc ttt gga ctc ttt ctt gtg aaa ccc gac aac	970	
112 Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp Asn		
113 295 300 305		
115 cca tgg gaa tgagaactat ccttcttgactccttagtt gctaagtccct	1019	
116 Pro Trp Glu		
119 caagctgcta tggggatgg ggtctgagca ggggtccctt ccattgacttt ctcttgcctt	1079	
121 taactggact tggatattat tctgagcata gctcagacaa gactttatat aattcactag	1139	
123 atagcattag taaaactgctg ggcagctgct agataaaaaaa aaatttctaa atcaaagttt	1199	
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129 <211> LENGTH: 309		
130 <212> TYPE: PRT		
131 <213> ORGANISM: Mus sp.		
133 <400> SEQUENCE: 2		

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135 Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His
136 1 5 10 15
139 Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr
140 20 25 30
143 Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr
144 35 40 45
147 Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg
148 50 55 60
151 Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His
152 65 70 75 80
155 Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Ile Ala
156 85 90 95
159 Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr
160 100 105 110
163 Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln
164 115 120 125
167 Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly
168 130 135 140
171 Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys
172 145 150 155 160
175 Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr
176 165 170 175
179 Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val
180 180 185 190
183 Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro
184 195 200 205
187 Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val
188 210 215 220
191 Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr
192 225 230 235 240
195 Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser
196 245 250 255
199 Trp Ser Gln Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly
200 260 265 270
203 Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu
204 275 280 285
207 Leu Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro
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211 Asp Asn Pro Trp Glu
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215 <210> SEQ ID NO: 3
216 <211> LENGTH: 1618
217 <212> TYPE: DNA
218 <213> ORGANISM: Homo sapiens
221 <220> FEATURE:
222 <221> NAME/KEY: CDS
223 <222> LOCATION: (4)..(765)
224 <223> OTHER INFORMATION: (clone: human 4-1BB-L (7A))
226 <400> SEQUENCE: 3

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231	cct	ccc	gcg	ccc	cgc	gct	cgc	gcc	tgc	cgc	gta	ctg	cct	tgg	gcc	ctg	96	
232	Pro	Pro	Ala	Pro	Arg	Ala	Arg	Ala	Cys	Arg	Val	Leu	Pro	Trp	Ala	Leu		
233						20				25						30		
235	gtc	gcg	ggg	ctg	ctg	ctg	ctg	ctg	ctc	gct	gcc	gcc	tgc	gcc	gtc	144		
236	Val	Ala	Gly	Leu	Ala	Ala	Ala	Cys	Ala	Val								
237						35				40						45		
239	tcc	ctc	gcc	tgc	ccc	tgg	gcc	gtg	tcc	ggg	gct	cgc	gcc	tcg	ccc	ggc	192	
240	Phe	Leu	Ala	Cys	Pro	Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly		
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243	tcc	gcg	gcc	agc	ccg	aga	ctc	cgc	gag	ggt	ccc	gag	ctt	tcg	ccc	gac	240	
244	Ser	Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp		
245						65			70							75		
247	gat	ccc	gcc	ggc	ctc	ttg	gac	ctg	cg	cag	ggc	atg	ttt	g	cg	cag	ctg	288
248	Asp	Pro	Ala	Gly	Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu		
249	80					85				90						95		
251	gtg	gcc	caa	aat	gtt	ctg	ctg	atc	gat	ggg	ccc	ctg	agc	tgg	tac	agt	336	
252	Val	Ala	Gln	Asn	Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser		
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257						115				120						125		
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263	tcc	ttt	caa	cta	gag	ctg	cg	cg	gt	gt	gcc	ggc	gag	ggc	tca	ggc	480	
264	Phe	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly		
265						145			150							155		
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271	gcc	gcc	gcc	ctg	gct	ttg	acc	gtg	gac	ctg	cca	ccc	gcc	tcc	tcc	gag	576	
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273						180				185						190		
275	gct	cgg	aac	tcg	gcc	tcc	gg	t	tc	cag	ggc	cgc	ttg	ctg	cac	ctg	agt	624
276	Ala	Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser		
277						195				200						205		
279	gcc	ggc	cag	cgc	ctg	ggc	gtc	cat	ttt	cac	act	gag	gcc	agg	gca	cgc	672	
280	Ala	Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg		
281						210			215							220		
283	cat	gcc	tgg	cag	ctt	acc	cag	ggc	gcc	aca	gtc	ttt	gga	ctc	tcc	cg	720	
284	His	Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg		
285						225			230							235		
287	gtg	acc	ccc	gaa	atc	cca	gcc	gga	ctc	cct	tca	ccg	agg	tcg	gaa		765	
288	Val	Thr	Pro	Glu	Ile	Pro	Ala	Gly	Leu	Pro	Ser	Pro	Arg	Ser	Glu			
289	240					245				250								
291	aac	ggcc	cag	ctg	gg	cag	cc	acc	ctg	gga	cag	gtc	ccg	atc	c	ttc	atg	825

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297	atatttattc	tgagccctgag	ctcagataat	atattatata	tattatata	atatatata	1005											
299	ttcttattaa	agaggatcct	gagtttgta	atggacttt	ttagaggagt	tgttttgggg	1065											
301	ggggggctt	cgacattgcc	gaggctggc	ttgaactcct	ggacttagac	gatccctcctg	1125											
303	cctcagcc	ccaagcaact	gggattcatc	cttttattta	attcattgtt	cttatttgcc	1185											
305	tatttgtgt	tattgagcat	ctgttatgt	ccagcattgt	gcccaggcta	gggggctata	1245											
307	gaaacatcta	gaaatagact	gaaagaaaat	ctgagttatg	gtaatacgtg	aggaatttaa	1305											
309	agactcatcc	ccagcctcca	cctcctgtgt	gatactggg	ggctagctt	tttctttctt	1365											
311	tctttttttt	gagatggct	tgttctgtca	accaggctag	aatgcagcgg	tgcaatcatg	1425											
313	agtcaatgca	gcctccagcc	tcgacctccc	gaggctcagg	tgatcctccc	atctcagcct	1485											
315	ctcgagtagc	tgggaccaca	gttgtgtgcc	accacactt	gctaactttt	taatttttt	1545											
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334					20				25						30			
337	Ala	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Cys	Ala	Val	Phe			
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341	Leu	Ala	Cys	Pro	Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly	Ser		
342					50				55						60			
345	Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	Asp		
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353	Ala	Gln	Asn	Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser	Asp		
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358						115				120					125			
361	Asp	Thr	Lys	Glu	Leu	Val	Val	Ala	Lys	Ala	Gly	Val	Tyr	Tyr	Val	Phe		
362						130				135					140			
365	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	Ser		
366						145				150			155		160			
369	Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly	Ala		
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373	Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu	Ala		
374							180				185				190			
377	Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser	Ala		
378						195				200					205			
381	Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg	His		
382						210				215					220			
385	Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg	Val		
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VERIFICATION SUMMARY

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